

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
 Yue, Henry
 Lal, Preeti
 Shah, Purvi
 Corley, Neil C.

(ii) TITLE OF THE INVENTION: PROTEINS ASSOCIATED WITH CELL PROLIFERATION

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 (B) STREET: 3174 Porter Dr.
 (C) CITY: Palo Alto
 (D) STATE: CA
 (E) COUNTRY: USA
 (F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
 (B) COMPUTER: IBM Compatible
 (C) OPERATING SYSTEM: DOS
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
 (B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
 (B) REGISTRATION NUMBER: 36,749
 (C) REFERENCE/DOCKET NUMBER: PF-0421 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
 (B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: SYNORAB01
 (B) CLONE: 358673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Phe	Gln	Ile	Pro	Glu	Phe	Glu	Pro	Ser	Glu	Gln	Glu	Asp	Ser	Ser
1				5				10						15	
Ser	Ala	Glu	Arg	Gly	Leu	Gly	Pro	Ser	Pro	Ala	Gly	Asp	Gly	Pro	Ser
			20				25						30		

Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala
 35 40 45
 Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala
 50 55 60
 Gly Ala Val Glu Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr
 65 70 75 80
 Glu Asp Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg
 85 90 95
 Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg
 100 105 110
 Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly
 115 120 125
 Leu Pro Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser
 130 135 140
 Ser Ser Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly
 145 150 155 160
 Arg Gly Ser Ser Ala Pro Ser Gln
 165

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: 358673
 (B) CLONE: SYNORAB01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGACCGTCCG	CGGGAGACTG	AGGTCCTGAG	CCGACAGCCT	CAGCTCCCTG	CCAGGCCAGA	60
CCCGGCAGAC	AGATGAGGGC	CCAGGAGGCC	TGGCGGGCCT	GGGGGCGCTA	CGGTGGGAGA	120
GGAAGCCAGG	GGTACCTGCC	TCTGCCTTCC	AGGGCCACCG	TTGGCCCCAG	CTGTGCCTTG	180
ACTACGTAAC	ATCTTGTCCT	CACAGCCCAG	AGCATGTTCC	AGATCCCAGA	GTTTGAGCCG	240
AGTGAGCAGG	AAGACTCCAG	CTCTGCAGAG	AGGGGCCTGG	GCCCCAGCCC	CGCAGGGGAC	300
GGGCCCTCAG	GCTCCGGCAA	GCATCATCGC	CAGGCCCCAG	GCCTCCTGTG	GGACGCCAGT	360
CACCAGCAGG	AGCAGCCAAC	CAGCAGCAGC	CATCATGGAG	GCGCTGGGGC	TGTGGAGATC	420
CGGAGTCGCC	ACAGCTCCTA	CCCCGCGGGG	ACGAGGAGCG	ACGAAGGGAT	GGGGGAGGAG	480
CCCAGCCCCT	TTCGGGGCCG	CTCGCGCTCG	GCGCCCCCCA	ACCTCTGGGC	AGCACAGCGC	540
TATGGCCGCG	AGCTCCGGAG	GATGAGTGAC	GAGTTTGTGG	ACTCCTTTAA	GAAGGGACTT	600
CCTCGCCCGA	AGAGCGCGGG	CACAGCAACG	CAGATGCGGC	AAAGCTCCAG	CTGGACGCGA	660
GTCTTCCAGT	CCTGGTGGA	TCGGAACCTG	GGCAGGGGAA	GCTCCGCCCC	CTCCCACTGA	720
CCTTCGCTCC	ACATCCCGAA	ACTCCACCCG	TTCCCACTGC	CCTGGGCAGC	CATCTTGAAT	780
ATGGGCGGAA	GTACTTCCCT	CAGGCCTATG	CAAAAAGAGG	ATCCGTGCTG	TCTCCTTTGG	840
AGGGAGGGCT	GACCCAGATT	CCCTTCCGGT	GCGTGTGAAG	CCACGGAAGG	CTTGGTCCCA	900
TCGGAAGTTT	TGGGT'TTTC	GCCCACAGCC	GCCGGAAGTG	GCTCCGTGGC	CCCGCCCTCA	960
GGCTCCGGGC	TTTCCCCCAG	GCGCCTGCGC	TAAGTCGCGA	GCCAGGTTTA	ACCGTTGCGT	1020
CACCGGGACC	CGAGCCCCCG	CGATGCCCTG	GGGGCCGTGC	TCACTACCAA	ATGTTAATAA	1080
AGCCCCGCGT	TGTGCAAAAA	AAAAA				1105

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LATRTUT02
 (B) CLONE: 1352286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Arg Val Val Thr Ile Val Ile Leu Leu Cys Phe Cys Lys Ala Ala
 1 5 10 15
 Glu Leu Arg Lys Ala Ser Pro Gly Ser Val Arg Ser Arg Val Asn His
 20 25 30
 Gly Arg Ala Gly Gly Gly Arg Arg Gly Ser Asn Pro Val Lys Arg Tyr
 35 40 45
 Ala Pro Gly Leu Pro Cys Asp Val Tyr Thr Tyr Leu His Glu Lys Tyr
 50 55 60
 Leu Asp Cys Gln Glu Arg Lys Leu Val Tyr Val Leu Pro Gly Trp Pro
 65 70 75 80
 Gln Asp Leu Leu His Met Leu Leu Ala Arg Asn Lys Ile Arg Thr Leu
 85 90 95
 Lys Asn Asn Met Phe Ser Lys Phe Lys Lys Leu Lys Ser Leu Asp Leu
 100 105 110
 Gln Gln Asn Glu Ile Ser Lys Ile Glu Ser Glu Ala Phe Phe Gly Leu
 115 120 125
 Asn Lys Leu Thr Thr Leu Leu Gln His Asn Gln Ile Lys Val Leu
 130 135 140
 Thr Glu Glu Val Phe Ile Tyr Thr Pro Leu Leu Ser Tyr Leu Arg Leu
 145 150 155 160
 Tyr Asp Asn Pro Trp His Cys Thr Cys Glu Ile Glu Thr Leu Ile Ser
 165 170 175
 Met Leu Gln Ile Pro Arg Asn Arg Asn Leu Gly Asn Tyr Ala Lys Cys
 180 185 190
 Glu Ser Pro Gln Glu Gln Lys Asn Lys Lys Leu Arg Gln Ile Lys Ser
 195 200 205
 Glu Gln Leu Cys Asn Glu Glu Lys Glu Gln Leu Asp Pro Lys Pro Gln
 210 215 220
 Val Ser Gly Arg Pro Pro Val Ile Lys Pro Glu Val Asp Ser Thr Phe
 225 230 235 240
 Cys His Asn Tyr Val Phe Pro Ile Gln Thr Leu Asp Cys Lys Arg Lys
 245 250 255
 Glu Leu Lys Lys Val Pro Asn Asn Ile Pro Pro Asp Ile Val Lys Leu
 260 265 270
 Asp Leu Ser Tyr Asn Lys Ile Asn Gln Leu Arg Pro Lys Glu Phe Glu
 275 280 285
 Asp Val His Glu Leu Lys Lys Leu Asn Leu Ser Ser Asn Gly Ile Glu
 290 295 300
 Phe Ile Asp Pro Ala Ala Phe Leu Gly Leu Thr His Leu Glu Glu Leu
 305 310 315 320
 Asp Leu Ser Asn Asn Ser Leu Gln Asn Phe Asp Tyr Gly Val Leu Glu
 325 330 335
 Asp Leu Tyr Phe Leu Lys Leu Leu Trp Leu Arg Asp Asn Pro Trp Arg
 340 345 350
 Cys Asp Tyr Asn Ile His Tyr Leu Tyr Tyr Trp Leu Lys His His Tyr
 355 360 365
 Asn Val His Phe Asn Gly Leu Glu Cys Lys Thr Pro Glu Glu Tyr Lys
 370 375 380
 Gly Trp Ser Val Gly Lys Tyr Ile Arg Ser Tyr Tyr Glu Glu Cys Pro
 385 390 395 400
 Lys Asp Lys Leu Pro Ala Tyr Pro Glu Ser Phe Asp Gln Asp Thr Glu
 405 410 415
 Asp Asp Glu Trp Glu Lys Lys His Arg Asp His Thr Ala Lys Lys Gln
 420 425 430
 Ser Val Ile Ile Thr Ile Val Gly
 435 440

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: LATRTUT02

(B) CLONE: 1352286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATGCAGCC CATTCTCTGG AGAACTTCCT CACACACCGC AGCAAAGAGA AGACTGAAAG 60
 ACAAACCTGG GTGCAGCCAG AGAGGTCCAG ATAGATGAGC TTGTGGCATC CATTCCCCAA 120
 GTTCAGCCTA GGGACTCCAC GTACCCACAG TGGGTCTCAT TGTTCCAGAA CTGCATTAGT 180
 TAAGATTACC CAGACTTGGA TTTCAAAGGA ATACTTTCAT TGTTCCGTCT GTAACACGAA 240
 GTAATTGGGG CCAGCTGGAT GTCAGGATGC GTGTGGTTAC CATTGTAATC TTGCTCTGCT 300
 TTTGCAAAGC GGCTGAGCTG CGCAAAGCAA GCCACGGCAG TGTGAGAAGC CGAGTGAATC 360
 ATGGCCGGGC GGGTGGAGGC CGGAGAGGCT CCAACCCGCT CAAACGCTAC GCACCAGGCC 420
 TCCCGTGTGA CGTGTACACA TATCTCCATG AGAAATACTT AGATTGTCAA GAAAGAAAAT 480
 TAGTTTATGT GCTGCCTGGT TGGCCTCAGG ATTTGCTGCA CATGCTGCTA GCAAGAAACA 540
 AGATCCGCAC ATTGAAGAAC AACATGTTTT CCAAGTTTAA AAAGCTGAAA AGCCTGGATC 600
 TGCAGCAGAA TGAGATCTCT AAAATTGAGA GTGAGGCGTT CTTTGGTTTA AACAACTCA 660
 CCACCTCTT ACTGCAGCAC AACAGATCA AAGTCTTGAC GGAGGAAGTG TTCATTTACA 720
 CACCTCTCTT GAGCTACCTG CGTCTTTATG ACAACCCCTG GCACTGTACT TGTGAGATAG 780
 AAACGCTTAT TTCAATGTTG CAGATTCCCA GGAACCGGAA TTTGGGGAAC TACGCCAAGT 840
 GTGAAAGTCC ACAAGAACAA AAAAATAAAA AACTGCGGCA GATAAAATCT GAACAGTTGT 900
 GTAATGAAGA AAAGGAACAA TTGGACCCGA AACCCTCAAGT GTCAGGGAGA CCCCCAGTCA 960
 TCAAGCCTGA GGTGGACTCA ACTTTTTGCC ACAATTATGT GTTTCCCAT ACAAACCTGG 1020
 ACTGCAAAAG GAAAGAGTTG AAAAAAGTGC CAAACAACAT CCCTCCAGAT ATTGTTAAAC 1080
 TTGACTTGTG ATACAATAAA ATCAACCAAC TTCGACCCAA GGAATTTGAA GATGTTTCATG 1140
 AGCTGAAGAA ATTAAACCTC AGCAGCAATG GCATTGAATT CATCGATCCT GCCGCTTTTT 1200
 TAGGGCTCAC ACATTTAGAA GAATTAGATT TATCAAACAA CAGTCTGCAA AACTTTGACT 1260
 ATGGCGTATT AGAAGACTTG TATTTTTTGA AACTCTTGTTG GCTCAGAGAT AACCTTGGA 1320
 GATGTGACTA CAACATTCAC TACCTCTACT ACTGGTTAAA GCACCACTAC AATGTCCATT 1380
 TTAATGGCCT GGAATGCAAA ACGCCTGAAG AATACAAAG ATGGTCTGTG GGAAAATATA 1440
 TTAGAAGTTA CTATGAAGAA TGCCCCAAAG ACAAGTTACC AGCATATCCT GAGTCATTTG 1500
 ACCAAGACAC AGAAGATGAT GAATGGGAAA AAAAACATAG AGATCACACC GCAAAGAAGC 1560
 AAAGCGTAAT AATTACTATA GTAGGATAAG GTAGAAATTG TTCTGATTGT AATTAGTTTT 1620
 GTATTTTCTA TACTGGTGTG AGAAAACATA TGTTTACATT TGATTAACCTG TGTTGCCTAT 1680
 TTATGCAGGG TAATCCAGCT AAAGGAAGCT TTCTTTAATT ATAAGTATTA TTGTGACTAT 1740
 TATAGTAATC AAGAGAATGC TATCATCCTG CTTGCCTGTC CATTGTGGA ACAGCATCTG 1800
 GTGATATGCA ATTCCACACT GGTAACTGTC AGCAGTTGGG TCCTAATGAT GGCATTAGAC 1860
 TTTTATAATG TCCTGTATAA ATGTTTTTAC TGCTTTTAGA AAATAAAGAA AAAAACTTG 1920
 GTTCATGTTT ACATGCCTTT CGATAGCTGT TTGTGCATAC TTAAAGATGA TCAAATGAT 1980
 TTTATACAAA TGCTGTTATA ATAAATGTC ATTCCCTACC CCTCTACTTT TTTTCAGTAA 2040
 GTCATCTTAT ACATTAAATA AATTTCCATT TCTGAAAAAA AA 2082

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT01
 (B) CLONE: 815087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asp Val Glu Asn Glu Gln Ile Leu Asn Val Asn Pro Ala Asp Pro
 1 5 10 15
 Asp Asn Leu Ser Asp Ser Leu Phe Ser Gly Asp Glu Glu Asn Ala Gly
 20 25 30
 Thr Glu Glu Val Lys Asn Glu Ile Asn Gly Asn Trp Ile Ser Ala Ser
 35 40 45
 Ser Ile Asn Glu Ala Arg Ile Asn Ala Lys Ala Lys Arg Arg Leu Arg
 50 55 60
 Lys Asn Ser Ser Arg Asp Ser Gly Arg Gly Asp Ser Val Ser Asp Ser
 65 70 75 80
 Gly Ser Asp Ala Leu Arg Ser Gly Leu Thr Val Pro Thr Ser Pro Lys

85 90 95
 Gly Arg Leu Leu Asp Arg Arg Ser Arg Ser Gly Lys Gly Arg Gly Leu
 100 105 110
 Pro Lys Lys Gly Gly Ala Gly Gly Lys Gly Val Trp Gly Thr Pro Gly
 115 120 125
 Gln Val Tyr Asp Val Glu Glu Val Asp Val Lys Asp Pro Asn Tyr Asp
 130 135 140
 Asp Asp Gln Glu Asn Cys Val Tyr Glu Thr Val Val Leu Pro Leu Asp
 145 150 155 160
 Glu Arg Ala Phe Glu Lys Thr Leu Thr Pro Ile Ile Gln Glu Tyr Phe
 165 170 175
 Glu His Gly Asp Thr Asn Glu Val Ala Glu Met Leu Arg Asp Leu Asn
 180 185 190
 Leu Gly Glu Met Lys Ser Gly Val Pro Val Leu Ala Val Ser Leu Ala
 195 200 205
 Leu Glu Gly Lys Ala Ser His Arg Glu Met Thr Ser Lys Leu Leu Ser
 210 215 220
 Asp Leu Cys Gly Thr Val Met Ser Thr Thr Asp Val Glu Lys Ser Phe
 225 230 235 240
 Asp Lys Leu Leu Lys Asp Leu Pro Glu Leu Ala Leu Asp Thr Pro Arg
 245 250 255
 Ala Pro Gln Leu Val Gly Gln Phe Ile Ala Arg Ala Val Gly Asp Gly
 260 265 270
 Ile Leu Cys Asn Thr Tyr Ile Asp Ser Tyr Lys Gly Thr Val Asp Cys
 275 280 285
 Val Gln Ala Arg Ala Ala Leu Asp Lys Ala Thr Val Leu Leu Ser Met
 290 295 300
 Ser Lys Gly Gly Lys Arg Lys Asp Ser Val Trp Gly Ser Gly Gly Gly
 305 310 315 320
 Gln Gln Ser Val Asn His Leu Val Lys Glu Ile Asp Met Leu Leu Lys
 325 330 335
 Glu Tyr Leu Leu Ser Gly Asp Ile Ser Glu Ala Glu His Cys Leu Lys
 340 345 350
 Glu Leu Glu Val Pro His Phe His His Glu Leu Val Tyr Glu Ala Ile
 355 360 365
 Ile Met Val Leu Glu Ser Thr Gly Glu Ser Thr Phe Lys Met Ile Leu
 370 375 380
 Asp Leu Leu Lys Ser Leu Trp Lys Ser Ser Thr Ile Thr Val Asp Gln
 385 390 395 400
 Met Lys Arg Gly Tyr Glu Arg Ile Tyr Asn Glu Ile Pro Asp Ile Asn
 405 410 415
 Leu Asp Val Pro His Ser Tyr Ser Val Leu Glu Arg Phe Val Glu Glu
 420 425 430
 Cys Phe Gln Ala Gly Ile Ile Ser Lys Gln Leu Arg Asp Leu Cys Pro
 435 440 445
 Ser Arg Gly Arg Lys Arg Phe Val Ser Glu Gly Asp Gly Gly Arg Leu
 450 455 460
 Lys Pro Glu Ser Tyr
 465

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT01
- (B) CLONE: 815087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACAGCTCGAG CTCGAGCCGC AAAACTGTCT GCAGACGTCA ATTCGCCCC CCTCCCCCTT 60
 GTGAGAACTC GCTACGTAGC CAGCAACTGT GTAGTGTCTA CAAATGATGA AAACGATCAG 120

AAATGCGATT AGGTGTCGGG GAAAAAAGGG TTTCCCCTGT TTTTAACTTG TATTTTTACT 180
 TTAATTGTTA CAATCTTGAT ATTCTTAACG TGACTTTTTT GGGAAACCAC CAAGTGCTTT 240
 TTAAGCAAGG AGTTACTGAT TCTGAAGGAA GATTTCCATT AGGTAATTTG TTTAATCAGT 300
 GCAAGCGAAA TTAAGGGAAA ATGGATGTAG AAAATGAGCA GATACTGAAT GTAAACCCTG 360
 CAGATCCTGA TAACCTAAGT GACTCTCTCT TTTCCGGTGA TGAAGAAAAT GCTGGGACTG 420
 AGGAAGTAAA GAATGAAATA AATGGAAATT GGATTTTCAGC ATCCTCCATT AACGAAGCTA 480
 GAATTAATGC CAAGGCAAAA AGGCGACTAA GGAAAACTC ATCCCGGGAC TCTGGCAGAG 540
 GCGATTCGGT CAGCGACAGT GGGAGTGACG CCCTTAGAAG TGGATTAAC TGTGCAACCA 600
 GTCCAAAGGG AAGGTTGCTG GATAGGCGAT CCAGATCTGG GAAAGGAAGG GGACTACCAA 660
 AGAAAGGTGG TGCAGGAGGC AAAGGTGTCT GGGGTACACC TGGACAGGTG TATGATGTGG 720
 AGGAGGTGGA TGTGAAAGAT CCTAACTATG ATGATGACCA GGAGAACTGT GTTTATGAAA 780
 CTGTAGTTTT GCCTTTGGAT GAAAGGGCAT TTGAGAAGAC TTTAACACCA ATCATAACAG 840
 AATATTTTGA GCATGGAGAT ACTAATGAAG TTGCGGAAAT GTTAAGAGAT TTAAATCTTG 900
 GTGAAATGAA AAGTGGAGTA CCAGTGTGG CAGTATCCTT AGCATTGGAG GGGAAGGCTA 960
 GTCATAGAGA GATGACATCT AAGCTTCTTT CTGACCTTTG TGGGACAGTA ATGAGCACAA 1020
 CTGATGTGGA AAAATCATTT GATAAATTGT TGAAAGATCT ACCTGAATTA GCACTGGATA 1080
 CTCCTAGAGC ACCACAGTTG GTGGGCCAGT TTATTGCTAG AGCTGTTGGA GATGGAATTT 1140
 TATGTAATAC CTATATTGAT AGTTACAAAG GAACGTGAGA TTGTGTGCAG GCTAGAGCTG 1200
 CTCTGGATAA GGCTACCGTG CTTCTGAGTA TGTCTAAAGG TGGAAAGCGT AAAGATAGTG 1260
 TGTGGGGCTC TGGAGGTGGG CAGCAATCTG TCAATCACCT TGTAAAGAG ATTGATATGC 1320
 TGCTGAAAGA ATATTTACTC TCTGGAGACA TATCTGAAGC TGAACATTGC CTTAAGGAAC 1380
 TGGAGTACC TCATTTTCAC CATGAGCTTG TATATGAAGC TATTATAATG GTTTTAGAGT 1440
 CAACTGGAGA AAGTACATTT AAGATGATTT TGGATTTATT AAAGTCCCTT TGGAGTCTT 1500
 CTACCATTAC TGTAGACCAA ATGAAAAGAG GTTATGAGAG AATTTACAAT GAAATTCCGG 1560
 ACATTAATCT GGATGTCCCA CATTCATACT CTGTGCTGGA GCGGTTTGTA GAAGAATGTT 1620
 TTCAGGCTGG AATAATTTCC AAACAACCTCA GAGATCTTTG TCCTTCAAGG GGCAGAAAGC 1680
 GTTTTGTAAG CGAAGGAGAT GGAGGTCGTC TTAAACCAGA GAGCTACTGA ATATAAGAAC 1740
 TCTTGCAGTC TTAGATGTTA TAAAAATATA TATCTGAATT GTAAGAGTTG TTAGCACAAG 1800
 TTTTTTTTTT TTTTTTTTTT TAAGCACTTG TTTTGGGTAC AAGGCATTTT TGACATTTTA 1860
 TAAACCTACA TTTAAGGGGA ATTTTAAAG GAAATGTTTT TTCTTTTTTT TTTGTTTTTC 1920
 GAGGGGGCAA GGAGGGACAG AAAAGTAACC TCTTCTTAAG TGGAAATATC TAATAAGCTA 1980
 CCTTTGTAA GTGCCATGTT TATTATCTAA TCATTCCAAG TTTTGCATTG ATGTCTGACT 2040
 GCCACTCCTT TCTTTCAAGG ACAGTGTTTT TTGTAGTAAA ATCACTGGTT TATACAAAGC 2100
 TTTATTTAGG GGGTAAAGTT AAGCTGCTAA AACCCTCATGT TGGCTGCTGC TGTGAGATA 2160
 CTGTGCTTTG GGAGTAAAAA AAGAAAGTTA TTTCTTTGTC TTAAAGAATT TTTAAAAAAT 2220
 TAGTCAATGAG ACTTATTCAT CTTTCCAGGG AACATACTGA TTGGTCTTAA AAGACTAGAC 2280
 AGTTAAGTAA AAGGTGGCTG GAACATCTAT TTTTCTACAA AACTGGAAAA ATGAACCTGG 2340
 TTCTAGAAGA ATGTACACCA AAATAAAACA TGTGAAGCAG TATTGAAAAA AAAAA 2395

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
 (B) CLONE: 1683637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Phe Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser
 1 5 10 15
 Ser Ala Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser
 20 25 30
 Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala
 35 40 45
 Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Arg
 50 55 60
 Trp Gly Cys Gly Asp Pro Glu Ser Pro Gln Leu Leu Pro Arg Gly Asp
 65 70 75 80
 Gly Gly Arg Arg Arg Asp Gly Gly Gly Ala Gln Pro Phe Arg Gly Arg
 85 90 95
 Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg

			100					105					110				
Glu	Leu	Arg	Arg	Met	Ser	Asp	Glu	Phe	Val	Asp	Ser	Phe	Lys	Lys	Gly		
		115					120					125					
Leu	Pro	Arg	Pro	Lys	Ser	Ala	Gly	Thr	Ala	Thr	Gln	Met	Arg	Gln	Ser		
	130					135					140						
Ser	Ser	Trp	Thr	Arg	Val	Phe	Gln	Ser	Trp	Trp	Asp	Arg	Asn	Leu	Gly		
145					150					155					160		
Arg	Gly	Ser	Ser	Ala	Pro	Ser	Gln										
				165													

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
 (B) CLONE: 1236329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Arg	Val	Val	Thr	Ile	Val	Ile	Leu	Leu	Cys	Phe	Cys	Lys	Ala	Ala		
1				5				10						15			
Glu	Leu	Arg	Lys	Ala	Ser	Pro	Gly	Ser	Val	Arg	Ser	Arg	Val	Asn	His		
		20					25						30				
Gly	Arg	Ala	Gly	Gly	Gly	Arg	Arg	Gly	Ser	Asn	Pro	Val	Lys	Arg	Tyr		
	35					40						45					
Ala	Pro	Gly	Leu	Pro	Cys	Asp	Val	Tyr	Thr	Tyr	Leu	His	Glu	Lys	Tyr		
50					55						60						
Leu	Asp	Cys	Gln	Glu	Arg	Lys	Leu	Val	Tyr	Val	Leu	Pro	Gly	Trp	Pro		
65					70					75					80		
Gln	Asp	Leu	Leu	His	Met	Leu	Leu	Ala	Arg	Asn	Lys	Ile	Arg	Thr	Leu		
			85					90						95			
Lys	Asn	Asn	Met	Phe	Ser	Lys	Phe	Lys	Lys	Leu	Lys	Ser	Leu	Asp	Leu		
		100					105						110				
Gln	Gln	Asn	Glu	Ile	Ser	Lys	Ile	Glu	Ser	Glu	Ala	Phe	Phe	Gly	Leu		
	115					120						125					
Asn	Lys	Leu	Thr	Thr	Leu	Leu	Gln	His	Asn	Gln	Ile	Lys	Val	Leu			
130					135					140							
Thr	Glu	Glu	Val	Phe	Ile	Tyr	Thr	Pro	Leu	Leu	Ser	Tyr	Leu	Arg	Leu		
145				150						155					160		
Tyr	Asp	Asn	Pro	Trp	His	Cys	Thr	Cys	Glu	Ile	Glu	Thr	Leu	Ile	Ser		
		165						170						175			
Met	Leu	Gln	Ile	Pro	Arg	Asn	Arg	Asn	Leu	Ala	Asn	Tyr	Ala	Lys	Cys		
		180						185					190				
Glu	Ser	Pro	Gln	Glu	Gln	Lys	Asn	Lys	Lys	Leu	Arg	Gln	Ile	Lys	Ser		
	195					200						205					
Glu	Gln	Leu	Cys	Asn	Glu	Glu	Glu	Lys	Glu	Gln	Leu	Asp	Pro	Lys	Pro		
210					215						220						
Gln	Val	Ser	Gly	Arg	Pro	Pro	Val	Ile	Lys	Pro	Glu	Val	Asp	Ser	Thr		
225				230						235					240		
Phe	Cys	His	Asn	Tyr	Val	Phe	Pro	Ile	Gln	Thr	Leu	Asp	Cys	Lys	Arg		
			245						250					255			
Lys	Glu	Leu	Lys	Lys	Val	Pro	Asn	Asn	Ile	Pro	Pro	Asp	Ile	Val	Lys		
		260					265						270				
Leu	Asp	Leu	Ser	Tyr	Asn	Lys	Ile	Asn	Gln	Leu	Arg	Pro	Lys	Glu	Phe		
	275				280							285					
Glu	Asp	Val	His	Glu	Leu	Lys	Lys	Leu	Asn	Leu	Ser	Ser	Asn	Gly	Ile		
	290				295						300						
Glu	Phe	Ile	Asp	Pro	Gly	Ser	Leu	Arg									
305					310												

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
 (B) CLONE: 1384078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asp Ile Glu Asn Glu Gln Thr Leu Asn Val Asn Pro Thr Asp Pro
 1 5 10 15
 Asp Asn Leu Ser Asp Ser Leu Phe Ser Gly Asp Glu Glu Asn Ala Gly
 20 25 30
 Thr Glu Glu Ile Lys Asn Glu Ile Asn Gly Asn Trp Ile Ser Ala Ser
 35 40 45
 Thr Ile Asn Glu Ala Arg Ile Asn Ala Lys Ala Lys Arg Arg Leu Arg
 50 55 60
 Lys Asn Ser Ser Arg Asp Ser Gly Arg Gly Asp Ser Val Ser Asp Asn
 65 70 75 80
 Gly Ser Glu Ala Val Arg Ser Gly Val Ala Val Pro Thr Ser Pro Lys
 85 90 95
 Gly Arg Leu Leu Asp Arg Arg Ser Arg Ser Gly Lys Gly Arg Gly Leu
 100 105 110
 Pro Lys Lys Gly Gly Ala Gly Gly Lys Gly Val Trp Gly Thr Pro Gly
 115 120 125
 Gln Val Tyr Asp Val Glu Glu Val Asp Val Lys Asp Pro Asn Tyr Asp
 130 135 140
 Asp Asp Gln Glu Asn Cys Val Tyr Glu Thr Val Val Leu Pro Leu Asp
 145 150 155 160
 Glu Thr Ala Phe Glu Lys Thr Leu Thr Pro Ile Ile Gln Glu Tyr Phe
 165 170 175
 Glu His Gly Asp Thr Asn Glu Val Ala Glu Met Leu Arg Asp Leu Asn
 180 185 190
 Leu Gly Glu Met Lys Ser Gly Val Pro Val Leu Ala Val Ser Leu Ala
 195 200 205
 Leu Glu Gly Lys Ala Ser His Arg Glu Met Thr Ser Lys Leu Leu Ser
 210 215 220
 Asp Leu Cys Gly Thr Val Met Ser Thr Asn Asp Val Glu Lys Ser Phe
 225 230 235 240
 Asp Lys Leu Leu Lys Asp Leu Pro Glu Leu Ala Leu Asp Thr Pro Arg
 245 250 255
 Ala Pro Gln Leu Val Gly Gln Phe Ile Ala Arg Ala Val Gly Asp Gly
 260 265 270
 Ile Leu Cys Asn Thr Tyr Ile Asp Ser Tyr Lys Gly Thr Val Asp Cys
 275 280 285
 Val Gln Ala Arg Ala Ala Leu Asp Lys Ala Thr Val Leu Leu Ser Met
 290 295 300
 Ser Lys Gly Gly Lys Arg Lys Asp Ser Val Trp Gly Ser Gly Gly Gly
 305 310 315 320
 Gln Gln Pro Val Asn His Leu Val Lys Glu Ile Asp Met Leu Leu Lys
 325 330 335
 Glu Tyr Leu Leu Ser Gly Asp Ile Ser Glu Ala Glu His Cys Leu Lys
 340 345 350
 Glu Leu Glu Val Pro His Phe His His Glu Leu Val Tyr Glu Ala Ile
 355 360 365
 Val Met Val Leu Glu Ser Thr Gly Glu Ser Ala Phe Lys Met Ile Leu
 370 375 380
 Asp Leu Leu Lys Ser Leu Trp Lys Ser Ser Thr Ile Thr Ile Asp Gln
 385 390 395 400
 Met Lys Arg Gly Tyr Glu Arg Ile Tyr Asn Glu Ile Pro Asp Ile Asn
 405 410 415



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